

SEQUENCE LISTING

TO740 5 (1) GENERAL INFORMATION:

(i) APPLICANT: Magal, Ella
Delaney, John M.10 (ii) TITLE OF INVENTION: METHOD FOR PREVENTING AND TREATING
HEARING LOSS USING A NEURTURIN PROTEIN PRODUCT

(iii) NUMBER OF SEQUENCES: 5

15 (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Amgen Inc.
(B) STREET: One Amgen Center Drive
(C) CITY: Thousand Oaks
(D) STATE: California
(E) COUNTRY: USA

20 (F) ZIP: 91320-1789

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.3025 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US
(B) FILING DATE: 29-JUN-1998
(C) CLASSIFICATION:30 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/054184
(B) FILING DATE: 30-JUL-199735 (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Curry, Daniel R.
(B) REGISTRATION NUMBER: 32,727
(C) REFERENCE/DOCKET NUMBER: A-444

(2) INFORMATION FOR SEQ ID NO:1:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

55 Ala Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg
1 5 10 1560 Val Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu Phe
20 25 3065 Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp Leu
35 40 45Gly Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg Val
50 55 60

Arg Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser
 65 70 75 80

5 Phe Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser Ala
 85 90 95

10 Arg Glu Cys Ala Cys Val
 100

(2) INFORMATION FOR SEQ ID NO:2:

- 15 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 20 (ii) MOLECULE TYPE: protein
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Pro Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser
 1 5 10 15

Glu Leu Gly Leu Gly Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr
 20 25 30

Cys Ala Gly Ala Cys Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu
 35 40 45

Arg Arg Leu Arg Gln Arg Arg Arg Val Arg Arg Glu Arg Ala Arg Ala
 50 55 60

35 His Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu
 65 70 75 80

40 Asp Val His Ser Arg Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu
 85 90 95

Cys Ala Cys Val
 100

45 (2) INFORMATION FOR SEQ ID NO:3:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 312 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
50 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: DNA (genomic)

55 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..309

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

60 ATG GCA CGT CTG GGT GCT CGT CCG TGT GGT CTG CGT GAA CTG GAA GTT
48 Met Ala Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val
65 1 5 10 15

75

CGT GTT TCC GAA CTG GGT CTG GGT TAC GCT TCC GAC GAA ACC GTT CTG
96 Arg Val Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu
5 20 25 30

TTC CGT TAC TGT GCA GGT GCT TGT GAA GCA GCT GCA CGT GTT TAC GAC
144 Phe Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp
10 35 40 45

CTG GGT CTG CGT CGC CTG CGT CAG CGC CGT CGC CTG CGT CGC GAA CGT
192 Leu Gly Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg
15 50 55 60

GTT CGC GCA CAG CCG TGT TGC CGT CCG ACC GCA TAC GAA GAC GAA GTT
240 Val Arg Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val
20 65 70 75 80

TCC TTC CTG GAC GCT CAC TCC CGT TAC CAC ACC GTT CAC GAA CTG TCC
288 Ser Phe Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser
25 85 90 95

GCA CGT CAC TGT GCG TGT GTT TAA
312 Ala Arg His Cys Ala Cys Val
30 100

(2) INFORMATION FOR SEQ ID NO:4:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

45 Met Ala Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val
1 5 10 15

Arg Val Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu
20 25 30

50 Phe Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp
35 40 45

Leu Gly Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg
55 50 55 60

Val Arg Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val
65 70 75 80

60 Ser Phe Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser
85 90 95

Ala Arg His Cys Ala Cys Val
100

65 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 amino acids
(B) TYPE: amino acid
5 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

15 Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser
1 5 10 15
Val Leu Ser Ile Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg
20 25 30
Leu Gly Pro Ala Leu Val Pro Leu His Arg Leu Pro Arg Thr Leu Asp
25 35 40 45
Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
25 50 55 60
Pro Asp Ala Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro
30 65 70 75 80
Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg Ala
35 85 90 95
Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val
40 100 105 110
35 Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu Phe Arg
115 120 125
45 Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp Leu Gly
130 135 140
Leu Arg Arg Leu Arg Gln Arg Arg Leu Arg Arg Glu Arg Val Arg
145 150 155 160
45 Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe
165 170 175
Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser Ala Arg
50 180 185 190
Glu Cys Ala Cys Val
195